

OIPe

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/761,117 TIME: 13:47:07

Input Set : A:\4377lapuy.app.txt
 Output Set: N:\CRF3\01292001\1761117.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Dalla-Favera, Riccardo
 7 Chaganti, Raju S.K.
 9 (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
 10 Dcl-6
 12 (iii) NUMBER OF SEQUENCES: 9
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Cooper & Dunham LLP
 16 (B) STREET: 1185 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: United States of America
 20 (F) ZIP: 10036
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/761,117
 C--> 30 (B) FILING DATE: 16-Jan-2001
 31 (C) CLASSIFICATION:
 33 (vii) ATTORNEY/AGENT INFORMATION:
 34 (A) NAME: White, John P.
 35 (B) REGISTRATION NUMBER: 28,678
 36 (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
 38 (ix) TELECOMMUNICATION INFORMATION:
 39 (A) TELEPHONE: (212) 278-0400
 40 (B) TELEFAX: (212) 391-0525
 41 (C) TELEX: 422523 COOP UI

Does Not Comply
 Corrected Diskette Needed
 See pp. 2-6

ERRORED SEQUENCES

44 (2) INFORMATION FOR SEQ ID NO: 1:
 46 (i) SEQUENCE CHARACTERISTICS:
 47 (A) LENGTH: 3720 base pairs
 48 (B) TYPR: nucleic acid
 49 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear
 52 (ii) MOLECULE TYPE: cDNA
 54 (ix) FEATURE:
 55 (A) NAME/KEY: CDS
 56 (B) LOCATION: 328..2445
 58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 E--> 60 GGCCCCTCGA GCTCTGAACC GGAACCTCCA AATTCGAGAC GCTCTGCTTA

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Input Set : A:\43771apuy_app.txt

Output Set : N:\CRF3\0129001\I761117.raw

```

61 TGAGGACCTC      60
E--> 63 GAAATAGCCG GGCCTGAGAA AAAATCTTAT GCCTTTGAGG GCTTTTGGTT
64 GCGCAGGGCG      129
E--> 66 AGTAAATATC ATCGAGAGCT GACACCAAGT CCTCCCTCG CACGTAGCAG
67 TCTAAATCTC      180
E--> 69 CGAAGCTCAA ATTTCGAGAA TTGAGCTCTG TTGATTCTTA GAACGGGGT
70 CTTTAGAGAT      240
E--> 72 GCGATGCA GAAGGCTCTA GGAAGGCCG GACACAGGT TTTGAGCRAA
73 ATTTTGACT      300
E--> 75 GTGAAGCAAG GCATTGGCTA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT
W--> 76 351
77 Met Ala Ser Pro Ala Asp Ser Cys
78 1 5
E--> 80 ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT
W--> 81 399
82 Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg
W--> 83 10 15 20
E--> 85 CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT
W--> 86 447
87 Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg
W--> 88 25 30 35 40
E--> 90 GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG
W--> 91 495
92 Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu
W--> 93 45 50 55
E--> 95 TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC
W--> 96 543
97 Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile
W--> 98 60 65 70
E--> 100 AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC
W--> 101 591
102 Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp
W--> 103 75 80 85
E--> 105 TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT
W--> 106 639
107 Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala
W--> 108 90 95 100
E--> 110 GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT
W--> 111 687
112 Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr
W--> 113 105 110 115 120
E--> 115 TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC
W--> 116 735
117 Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile
W--> 118 125 130 135
E--> 120 AAG CCT CCT CGT GAA GAG TTC CTC AAC ACG CGG ATG CTG ATG CCC CAA
W--> 121 783
122 Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln
W--> 123 140 145 150

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Wrapped nucleic
acids. The text
or numbers have
"wrapped" down to
the next line.

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```

E--> 125 GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA
W--> 126 831
127 Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro
W--> 128 155 160 165
E--> 130 CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG
W--> 131 879
132 Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu
W--> 133 170 175 180
E--> 135 TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC AGT TAC AGC CAC
W--> 136 927
137 Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His
W--> 138 185 190 195
E--> 140 CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC
W--> 141 975
142 Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val
W--> 143 205 210 215
E--> 145 CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT
W--> 146 1023
147 Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys
W--> 148 220 225 230
E--> 150 GAT AGT GCC AGG CCA CTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG
W--> 151 1071
152 Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu
W--> 153 235 240 245
E--> 155 GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA
W--> 156 1119
157 Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr
W--> 158 250 255 260
E--> 160 ATC CCA GAA GAG GCA CGA AGT GAT ATG CAC TAC AGT GTG GCT GAG GGC
W--> 161 1167
162 Ile Pro Glu Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Gly
W--> 163 265 270 275 280
E--> 165 CTC AAA CCT GCT GCC CCC TCA GCC CGA AAT GCC CCC TAC TTC CTT TGT
W--> 166 1215
167 Leu Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys
W--> 168 285 290 295
E--> 170 GAC AAG GCC AGC AAA GAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT
W--> 171 1263
172 Asp Lys Ala Ser Lys Glu Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile
W--> 173 300 305 310
E--> 175 GCC CTG CAT TTC GAG CCC CCC AAT GCA CCC CTG AAC CGG AAG GGT CTG
W--> 176 1311
177 Ala Leu His Phe Glu Pro Pro Asn Ala Pro Leu Asn Arg Lys Gly Leu
W--> 178 315 320 325
E--> 180 GTT AGT CCA CAG AGC CCC CAG AAA TCT GAC TGC CAG CCC AAC TCG CCC
W--> 181 1359
182 Val Ser Pro Glu Ser Pro Glu Lys Ser Asp Cys Glu Pro Asn Ser Pro
W--> 183 330 335 340
E--> 185 ACA GAG GCC TGC AGC AGT AAG AAT GCC TGC ATC CTC CAG GGT TCT GGC

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```

W--> 186 1407
187 Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Gln Gly Ser Gly 360
188 145 350
W--> 188 145 350
190 TCC CCT CCA GCC AAG AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AAG
W--> 191 1455
192 Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Trp Lys 375
193 365
E--> 195 AAA TAC AAG TTC ATC GTG CTC AAC AGC CTC AAC CAG AAT GCC AAA CCA
W--> 196 1503
197 Lys Tyr Lys Phe Ile Val Leu Asn Ser Leu Asn Gln Asn Ala Lys Pro 390
198 380
W--> 198 380
200 GGG GGG CCT GAG CAG GCT GAG CTG GGC CGC CTT TCC CCA CGA GCC TAC
W--> 201 1551
202 Gly Gly Pro Glu Gln Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr 405
203 400
W--> 203 400
205 ACG GCC CCA CCT GCC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTT GAC
E--> 206 1599
207 Thr Ala Pro Pro Ala Cys Gln Pro Pro Met Glu Pro Glu Asn Leu Asp 420
208 415
W--> 208 415
210 CTC CAG TCC CCA AAG AGC CTG AGT GCC AGC GGG GAG GAC TCC ACC ATC
E--> 211 1647
212 Leu Gln Ser Pro Thr Lys Leu Ser Ala Ser Gly Glu Asp Ser Thr Ile 440
213 430
W--> 213 425
215 CCA CAA GCC AGC CGG CTC AAT AAC ATC GTT AAC AGG TCC ATG ACG GGC
E--> 216 1695
217 Pro Gln Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly 455
218 445
W--> 218 445
220 TCT CCC CGC AGC AGC AGC GAG AGC CAC TCA CCA CTC TAC ATG CAC CCC
E--> 221 1743
222 Ser Pro Arg Ser Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro 470
223 460
W--> 223 460
225 CCG AAG TGC ACG TCC TGC GGC TCT CAG TCC CCA CAG CAT GCA GAG ATG
E--> 226 1791
227 Pro Lys Cys Thr Ser Cys Gly Ser Gln Ser Pro Gln His Ala Glu Met 485
228 475
W--> 228 475
230 TGC CTC CAC ACC GCT GGC CCC ACG TTC GCT GAG GAG ATG GGA GAG ACC
E--> 231 1839
232 Cys Leu His Thr Ala Gly Pro Thr Phe Ala Glu Glu Met Gly Glu Thr 500
233 490
W--> 233 490
235 CAG TCT GAG TAC TCA GAT TCT AGC TGT GAG AAC GGC GCC TTC TTC TGC
E--> 236 1887
237 Gln Ser Glu Tyr Ser Asp Ser Ser Cys Glu Asn Gly Ala Phe Phe Cys 520
238 505
W--> 238 505
240 AAT GAG TGT GAC TGC CGC TTC TCT GAG GAG GCC TCA CTC AAG AGG CAC
E--> 241 1935
242 Asn Glu Cys Asp Cys Arg Phe Ser Glu Glu Ala Ser Leu Lys Arg His 535
243 525
W--> 243 525
245 ACG CTG CAG ACC CAC AGT GAC AAA CCC TAC AAG TGT GAC CGC TGC CAG
E--> 246 1983
246 535

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1/29/01

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```

      247 Thr Leu Gln Thr His Ser Asp Lys Pro Tyr Lys Cys Asp Arg Cys Gln
W--> 248          540          545          550
E--> 250 GCC TCC TTC CGC TAC AAG GGC AAC CTC GCC AGC CAC AAG ACC GTC CAT
W--> 251 2031
      252 Ala Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Lys Thr Val His
W--> 253          555          560          565
E--> 255 ACC GGT GAG AAA CCC TAT CGT TGC AAC ATC TGT GGG GCC CAG TTC AAC
W--> 256 2079
      257 Thr Gly Glu Lys Pro Tyr Arg Cys Asn Ile Cys Gly Ala Gln Phe Asn
W--> 258          570          575          580
E--> 260 CGG CCA GCC AAC CTG AAA ACC CAC ACT CGA ATT CAC TCT GGA GAG AAG
W--> 261 2127
      262 Arg Pro Ala Asn Leu Lys Thr His Thr Arg Ile His Ser Gly Glu Lys
W--> 263 585          590          595          600
E--> 265 CCC TAC AAA TGC GAA ACC TGC GGA GCC AGA TTT GTA CAG GTG GCC CAC
W--> 266 2175
      267 Pro Tyr Lys Cys Glu Thr Cys Gly Ala Arg Phe Val Gln Val Ala His
W--> 268          605          610          615
E--> 270 CTC CGT GCC CAT GTC CTT ATC CAC ACT GGT GAG AAG CCC TAT CCC TGT
W--> 271 2223
      272 Leu Arg Ala His Val Leu Ile His Thr Gly Glu Lys Pro Tyr Pro Cys
W--> 273          620          625          630
E--> 275 GAA ATC TGT GGC ACC CGT TTC CGG CAC CTT CAG ACT CTG AAG ACC CAC
W--> 276 2271
      277 Glu Ile Cys Gly Thr Arg Phe Arg His Leu Gln Thr Leu Lys Ser His
W--> 278          635          640          645
E--> 280 CTG CGA ATC CAC ACA GGA GAG AAA CCT TAC CAT TGT GAG AAG TGT AAC
W--> 281 2319
      282 Leu Arg Ile His Thr Gly Glu Lys Pro Tyr His Cys Glu Lys Cys Asn
W--> 283          650          655          660
E--> 285 CTC CGT TTC CGT CAC AAA AGC CAG CTG CGA CTT CAC TTG CGC CAG AAG
W--> 286 2367
      287 Leu His Phe Arg His Lys Ser Glu Leu Arg Leu His Leu Arg Gln Lys
W--> 288 665          670          675          680
E--> 290 CAT GGC GCC ATC ACC AAC ACC AAG GTG CAA TAC CGC GTG TCA GCC ACT
W--> 291 2415
      292 His Gly Ala Ile Thr Asn Thr Lys Val Gln Tyr Arg Val Ser Ala Thr
W--> 293          685          690          695
E--> 295 GAC CTG CCT CCG GAG CTC CCC AAA GCC TGC TGAAGCATGG AGTGTGATGG
W--> 296 2465
      297 Asp Leu Pro Pro Glu Leu Pro Lys Ala Cys
W--> 298          700          705
E--> 300 CTTTCCTCTC CAGCCCCCTC TCAGAACTCA CCCAAGGAT ACTGTAAAC
      301 TTTCGAATCT 2525
E--> 303 TCATCCCATG ATGTAGTGCC TTTCATCTC ACTAGTGCAA ATCATAGCTG
      304 GGGTGGGG 2585
E--> 306 GTGTGGGGGG TCGGGGCTG GGGGACTGG AGCCCGACGA GCTCCCCCTC
      307 CCCCATGCC 2645
E--> 309 ATAAACATT AAGAAATCA TATTCCTCT TCTCCTATG GNNNNNNNN

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```

110 NNNNNNNNNN      2785
E--> 312 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
313 NNNNNNNNNN      2785
E--> 315 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
316 NNNNNNNNNN      2825
E--> 318 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
319 NNNNNNNNNN      2885
E--> 321 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
322 NNNNNNNNNN      2945
E--> 324 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
325 NNNNNNNNNN      3005
E--> 327 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
328 NNNNNNNNNN      3065
E--> 330 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
331 NNNNNNNNNN      3125
E--> 333 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
334 NNNNNNNNNN      3185
E--> 336 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
337 NNNNNNNNNN      3245
E--> 339 NTTTAAGTAT TGCATCTGTA TAAGTAAGAA AATATTTGT CTAAAAAGCC
340 TCAGTGTATT      3305
E--> 342 TGTATTTTTT TGCAAGTGGG GGGTTCAAT TTACCCAGTG TGTATTAATA
343 AAAACCCAAA      3365
E--> 345 GAACCCAAA ATCTCCAGAA GAAAAAATGT GTATTTTGT TCTAGTTTTC
346 AGTTTGATA      3425
E--> 348 TACCCGTACA ACGTGTCTTC ACGTGCCTT TTTTCACGA AGTTTCAAT
349 GATGGGCGAG      3485
E--> 351 CGTGACCAT CCCTTTTGA AGTGAGGA GACACAGGA CTGGAAGTG
352 TTACTACTA      3545
E--> 354 AACTCTCTTT GGAATGTTT GTCTCATCC ANTCGCTC ATGCTTGTT
355 GATACTACT      3605
E--> 357 CCGAGACAG GGTTCGCTG TGCTAAACT GCATTACGC GTGTAAAAA
358 ATAGCTGTAC      3665
E--> 360 CATATATAGA ATAAATCTT GGAAGTCGC AAAAAAATA AAAAAAATA
361 AAAA      3720

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VERIFICATION SUMMARY
 PATENT APPLICATION: US/09/761,117
 DATE: 01/29/2001
 TIME: 13:47:08
 Input Set : A:\4377\lapuy.app.txt
 Output Set : N:\CRF3\01292001\1761117.raw

Input Set : A:\4377\lapuy.app.txt
 Output Set : N:\CRF3\01292001\1761117.raw

L:29 M:220 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:]
 L:30 M:220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]
 L:60 M:254 E: No. of bases conflict, Input:0 Counted:50 SEQ:1
 M:254 Repeated in SeqNo=1
 L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1